

**Forensic Genetics Symposium**  
Organized with the Rio de Janeiro Court of Justice  
Rio de Janeiro, Brazil  
5 May 2017

IV Simpósio Internacional de Identificação Humana por DNA - Rio de Janeiro

# **Current Challenges Facing Forensic Genetics**

**John M. Butler, Ph.D.**

*NIST Fellow & Special Assistant to the Director for Forensic Science*  
U.S. National Institute of Standards and Technology

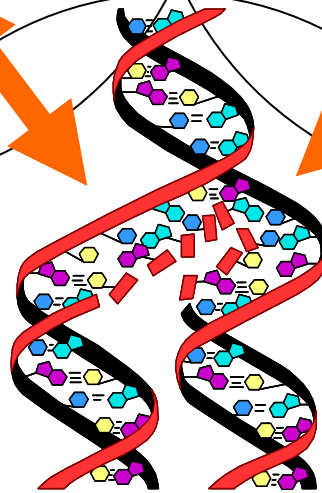
**Talk presented by Dr. Mecki Prinz**  
John Jay College of Criminal Justice,  
New York City, United States of America

# Communication Across the Criminal Justice System is Important

**Law  
Enforcement**



**Judicial**



**Laboratory**

*What Every Law  
Enforcement  
Officer Should  
Know About*

**DNA  
Evidence**





# TRAINING *Forensic DNA for Officers of the Court*

[Home](#) | [Glossary](#) | [Resources](#)

<https://forensic.training.nij.gov/>

- + 01 Introduction
- + 02 Biology of DNA
- + 03 Practical Issues Specific to DNA Evidence
- + 04 Introduction to the Forensic DNA Laboratory
- + 05 Assuring Quality in DNA Testing
- + 06 Understanding a Forensic DNA Lab Report
- + 07 Statistics and Population Genetics
- + 08 Mitochondrial DNA & Y-STR Analysis
- + 09 Forensic DNA Databases
- + 10 Collection of DNA Evidence from Suspects and Arrestees
- + 11 Pretrial DNA Evidence Issues
- + 12 Victim Issues
- + 13 Trial Presentation
- + 14 Postconviction DNA Cases
- + 15 Emerging Trends

## Login

### Security Upgrades

You should already have noticed and agreed to a new disclaimer made to make our registration process and courses more secure.

- Your password must now be at least 8 characters and include letters, numbers, and special characters (e.g., ~!@&#\$%^&#').
- You will be asked to reset your password every 90 days.
- You may not reuse any of your past 6 passwords.

### Please Login

Username

Password

Login

Don't have an account? [Register Now](#)

Forgot your username? [Retrieve your username](#) now.

# Butler Books on Forensic DNA Typing

2015



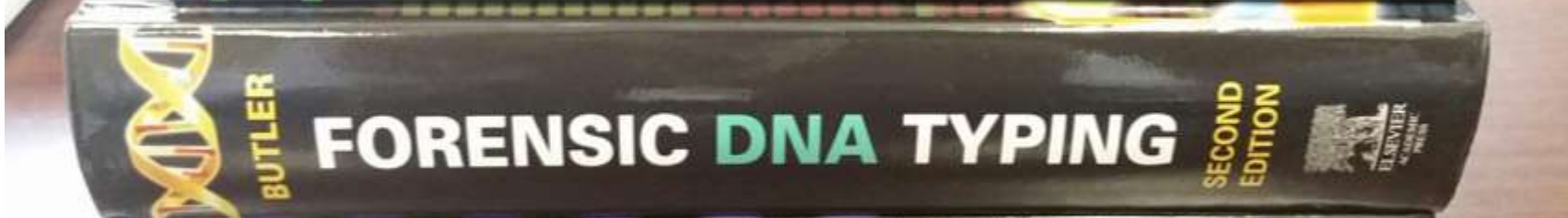
2012



2010



2005



2001



# National Institute of Standards and Technology

- Science agency **part of the U.S. Department of Commerce**
  - Started in 1901 as the **National Bureau of Standards**
  - Name changed in 1988 to the **National Institute of Standards and Technology (NIST)**
  - Forensic science research activities dating back to 1920s
  - Partnership since 2013 with U.S. Department of Justice to create the National Commission on Forensic Science (NCFS) and the Organization of Scientific Area Committees (OSAC)
- 
- Primary campus in Gaithersburg, Maryland (near Washington, D.C.)
  - >3,400 employees and >3,700 associates
  - Supplies >1300 reference materials
  - Defines official time for the U.S.

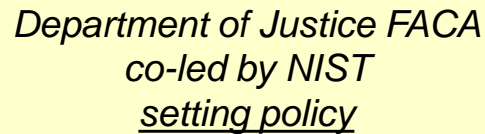


DNA reference material



# Partnership with Department of Justice

Charter completed on April 23, 2017



## NIST Funded Internal Research Programs

[illegible]

*NIST-administered*  
**>540 members of the community**  
*establishing standards and best practices*

**CoE: ~\$4M/year invested for  
5 years (2015-2020)**

432 participants (11 countries)

# Forensic Conference Organized by NIST

FORENSIC SCIENCE  
ERROR MANAGEMENT

INTERNATIONAL  
FORENSICS SYMPOSIUM

JULY 20-24, 2015 • WASHINGTON, DC



**Planning has started for a second Symposium**

**Date: July 24-28, 2017**

**Location: Gaithersburg, MD**

**Sponsors that have been approached**

**DoD, FBI, NIST**

[http://www.nist.gov/director/international\\_forensics\\_home.cfm](http://www.nist.gov/director/international_forensics_home.cfm)

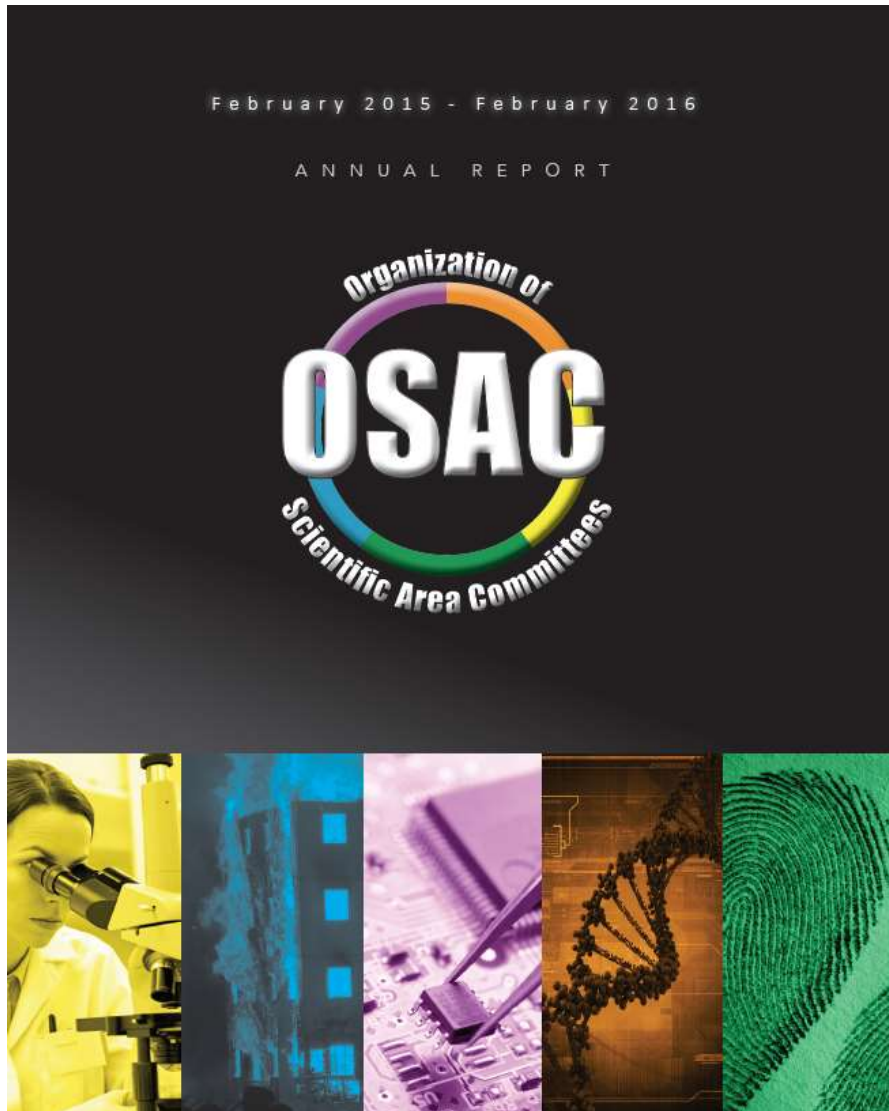


**>600 people involved in 34 operational units**  
<http://www.nist.gov/forensics/osac/index.cfm>

- Provides technical leadership to help develop and promulgate **consensus-based documentary standards and guidelines** for forensic science
- Promotes standards and guidelines that are **fit-for-purpose** and **based on sound scientific principles**
- Promotes the use of OSAC documents by accreditation and certification bodies
- Establishes and maintains working relationships with similar organizations



# OSAC Annual Report



- **74 page report** summarizing activities from the first year of OSAC (Feb 2015 to Feb 2016)
- Available as a pdf file for download at [https://www.nist.gov/sites/default/files/documents/2016/09/13/osac\\_annual\\_report\\_2015-2016.pdf](https://www.nist.gov/sites/default/files/documents/2016/09/13/osac_annual_report_2015-2016.pdf)

# DNA Capabilities to Aid Forensic Investigations

1. The **ability to identify the perpetrator**
2. Weight-of-evidence based on established genetic principles and statistics (Hardy-Weinberg 1908)
3. Established characteristics of genetic inheritance enables close **biological relatives** to be used for reference points using kinship associations
4. Superb **sensitivity** with PCR amplification (opens the possibility for contamination)
5. Well-established **quality assurance measures**
6. New **technology development** aided by genomics

Successful interpretation of DNA (Q-to-K comparison) depends on quality of the crime scene evidence (Q) and availability of suitable reference samples (K)



**Professor Peter Gill**

# Concerns have been Raised over Potential for DNA Contamination

Previous articles by Peter Gill on this topic:

- Gill, P. (1997). The utility of 'substrate controls' in relation to 'contamination'. *Forensic Science International*, 85(2):105-111.
- Gill, P., & Kirkham, A. (2004). Development of a simulation model to assess the impact of contamination in casework using STRs. *Journal of Forensic Sciences*, 49(3): 485-491.
- Gill, P., et al. (2010). Manufacturer contamination of disposable plastic-ware and other reagents—an agreed position statement by ENFSI, SWGDAM and BSAG. *Forensic Science International: Genetics*, 4(4): 269-270.



**Discusses the Amanda Knox case DNA results**

June 2014; 100 pages

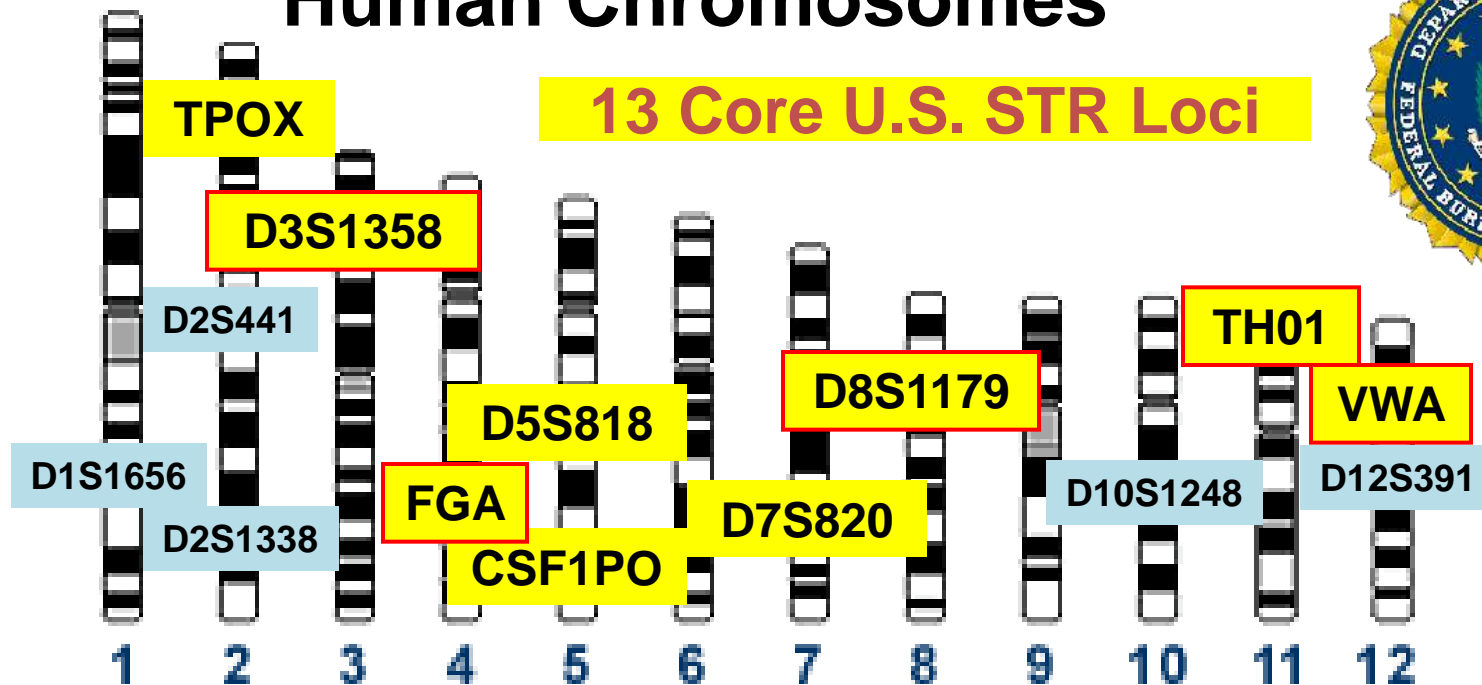
# Forensic DNA Testing in the United States

- We have **~200 public (state and local government) laboratories** performing forensic DNA analysis
  - Two large private companies (Bode Cellmark and Sorenson Forensics) and a few smaller ones perform forensic DNA analysis
- Over 15 million DNA profiles in the national DNA database (NDIS: National DNA Index System) run by the FBI Laboratory
  - Since 1998, the U.S. has included 13 core STR (short tandem repeat) markers; starting in 2017, this number has increased to 20 required STR loci
- Laboratories have many different protocols and in some cases, submitting the same sample to two different laboratories could result in two different results
  - Efforts are underway to improve standardization in the field

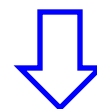
# Position of Forensic STR Markers on Human Chromosomes



## 13 Core U.S. STR Loci

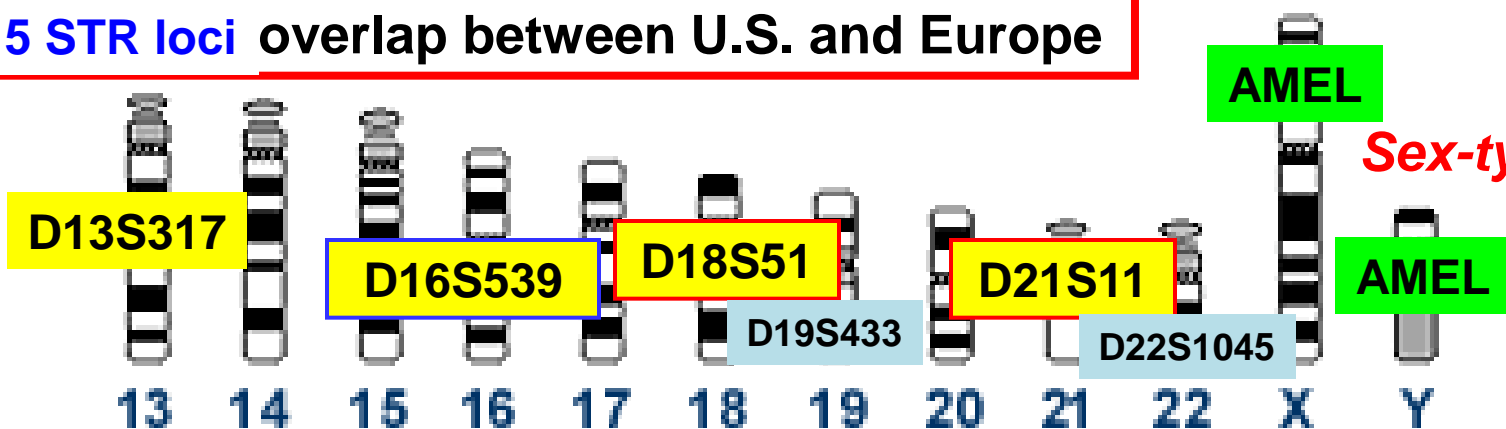


1997  
(13 loci)



2017  
(20 loci)

15 STR loci overlap between U.S. and Europe



*Sex-typing*

Core STR Loci for the United States



# Checks and Controls on Forensic DNA Results

Community	FBI DNA Advisory Board's Quality Assurance Standards ( <i>also interlaboratory studies</i> )
Laboratory	ASCLD/LAB, ANAB, A2LA Audits and Accreditation
Analyst	Proficiency Tests & Continuing Education
Method/Instrument	<b>Validation of Analytical Performance</b> (with aid of <b>traceable reference materials</b> )
Protocol	Standard Operating Procedure is followed
Data Sets	Allelic ladders, positive and negative amplification controls, and reagent blanks are used
Individual Sample	Internal size standard present in every sample
Interpretation of Result	<b>Second review by qualified analyst/supervisor</b>
Court Presentation of Evidence	Defense attorneys and experts with power of discovery requests

# Thoughts on the Future of Forensic DNA Published in 2015

PHILOSOPHICAL  
TRANSACTIONS B

[rstb.royalsocietypublishing.org](http://rstb.royalsocietypublishing.org)

Opinion piece



**Cite this article:** Butler JM. 2015 The future of forensic DNA analysis. *Phil. Trans. R. Soc. B* **370**: 20140252.

<http://dx.doi.org/10.1098/rstb.2014.0252>

Accepted: 26 February 2015

One contribution of 15 to a discussion meeting issue 'The paradigm shift for UK forensic science'.

## The future of forensic DNA analysis

John M. Butler

National Institute of Standards and Technology, Gaithersburg, MD, USA

The author's thoughts and opinions on where the field of forensic DNA testing is headed for the next decade are provided in the context of where the field has come over the past 30 years. Similar to the Olympic motto of 'faster, higher, stronger', forensic DNA protocols can be expected to become more rapid and sensitive and provide stronger investigative potential. New short tandem repeat (STR) loci have expanded the core set of genetic markers used for human identification in Europe and the USA. Rapid DNA testing is on the verge of enabling new applications. Next-generation sequencing has the potential to provide greater depth of coverage for information on STR alleles. Familial DNA searching has expanded capabilities of DNA databases in parts of the world where it is allowed. Challenges and opportunities that will impact the future of forensic DNA are explored including the need for education and training to improve interpretation of complex DNA profiles.

**Addressed Rapid DNA and  
Next-Generation Sequencing**

# Stages of Forensic DNA Progression

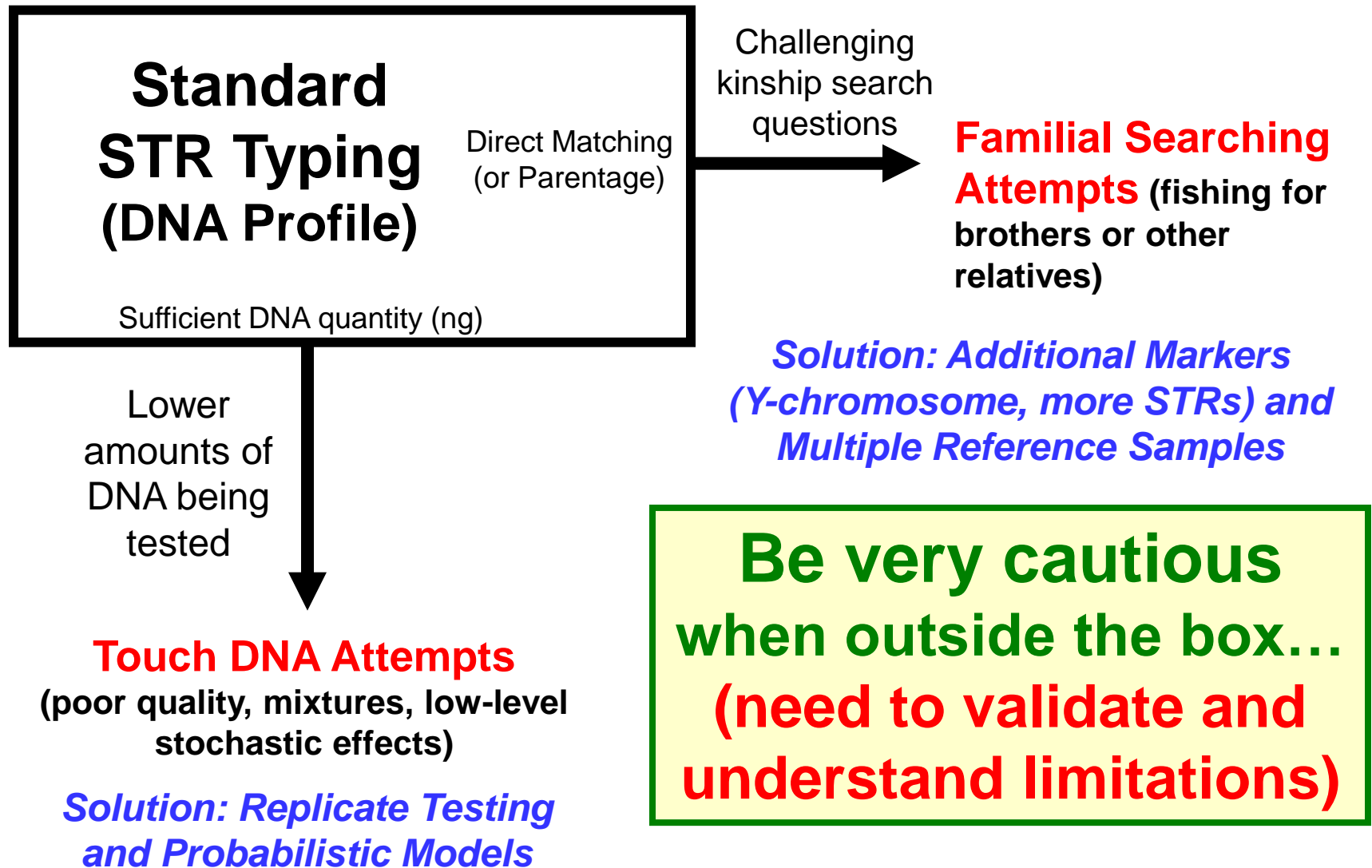
Stages	Time Frame	Description
<b>Exploration</b>	1985 - 1995	Beginnings, different methods tried (RFLP and early PCR)
<b>Stabilization</b>	1995 - 2005	Standardization to STRs, selection of core loci, implementation of Quality Assurance Standards
<b>Growth</b>	2005 - 2015	Rapid growth of DNA databases, extended applications pursued
<i>Sophistication</i>	<i>2015 to 2025 and beyond</i>	<i>Expanding tools available, confronting privacy concerns</i>

# Critical Challenges Faced Today

- **Success of DNA testing** → significant growth in sample submissions → sample backlogs
  - Laboratory automation and expert system data review
  - Restrictive case acceptance policies to avoid law enforcement investigator ‘swab-athons’ at crime scenes
- **Greater detection sensitivity** → more complex DNA mixtures and low-template DNA with ‘touch’ evidence
  - Probabilistic genotyping to cope with increase in data interpretation uncertainty
  - Use of a complexity threshold to avoid “skating on thin ice”

# Going Beyond the Core Competencies of Forensic DNA Testing...

## *Core Competency*





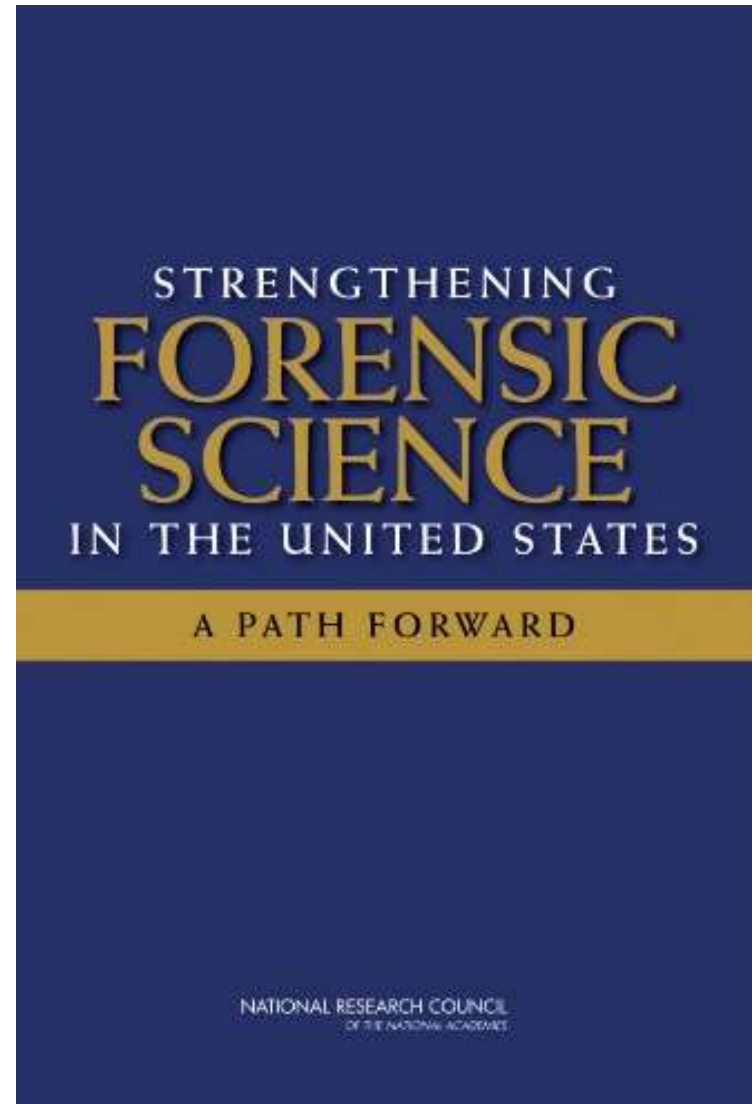
# Landmark Report Gives DNA Testing a Pass

Released February 18, 2009

The U.S. National Research Council of the National Academies issued a major report on forensic science in Feb. 2009.

*“With the exception of nuclear DNA analysis, no forensic method has been rigorously shown to have the capacity to consistently, and with a high degree of certainty, demonstrate a connection between evidence and a specific individual or source.” (p. 41)*

p. 100 mentions limitations with DNA mixtures



# PCAST Report Comments on Forensic DNA

Released September 20, 2016

- Supports appropriate use of single-source and simple mixture DNA analysis
- **Expresses reservations with complex DNA mixtures** ( $\geq 3$  contributors)

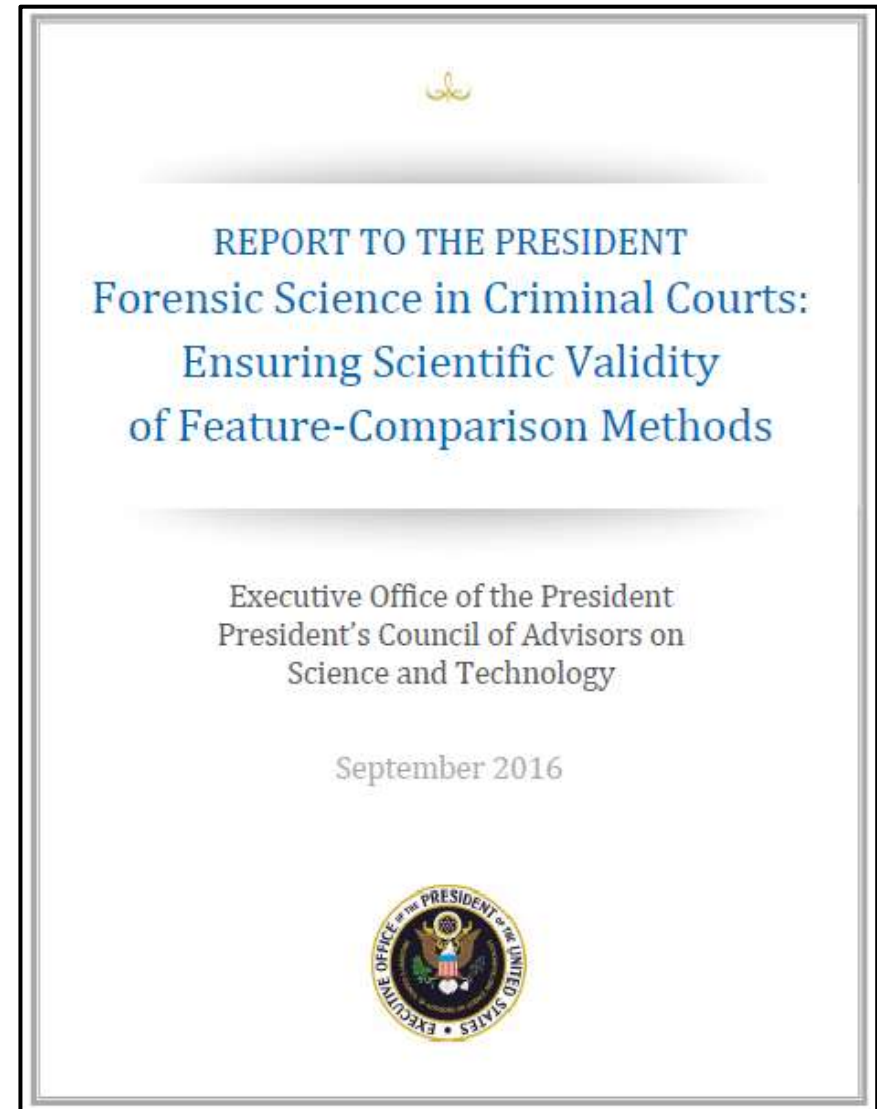
## PCAST Co-Chairs



Eric Lander



John Holdren



International conference

# *The hidden side of DNA profiles. Artifacts, errors and uncertain evidence*

Auditorium, Università Cattolica del Sacro Cuore  
Rome, 27-28 April, 2012



**David Balding:** “Low-template DNA cases are coming to court with limited abilities for sound interpretation. ... There are dangers with LTDNA but we know how to handle and manage them. Unfortunately, proper management is not a universal practice.”



**Peter Schneider:** “If you cannot explain your evidence to someone that is not from the field (like a judge) – and you need a lot of technical excuses to report something – then the result is not good. You should leave it on your desk and not take it to court. This is a very common sense approach to this problem.”

# Information from Chapter 7

## *Advanced Topics in Forensic DNA Typing: Interpretation*

### CHAPTER

# 7

## Low-Level DNA and Complex Mixtures

*“The limits of each DNA typing procedure should be understood, especially when the DNA sample is small, is a mixture of DNA from multiple sources, or is contaminated with interfering substances.”*

NRC I, 1992, p. 8

*“For the complex DNA profile, there is no predominant or overarching standard interpretation method.”*

Peter Gill ([Gill et al. 2012](#), report to the UK Forensic Science Regulator, p. 18)

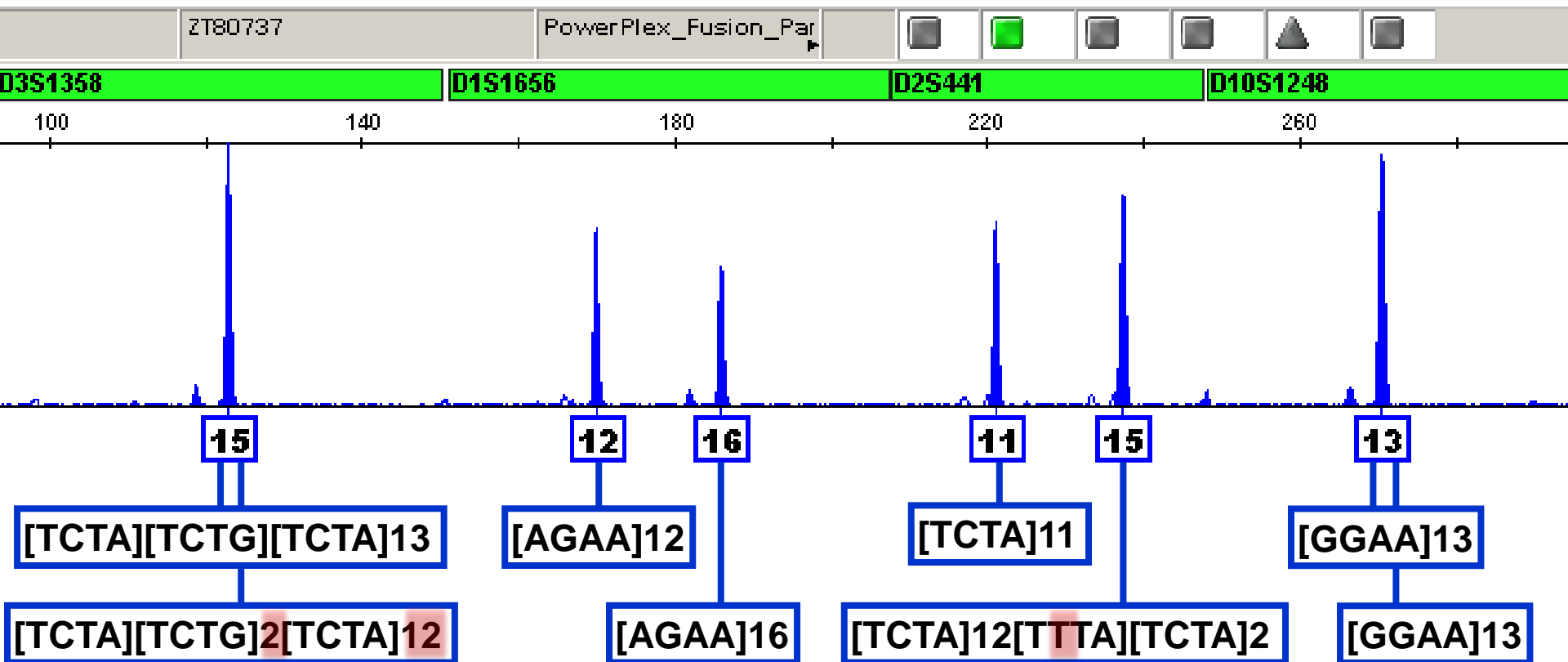
**“The limits of each DNA typing procedure should be understood, especially when the DNA sample is small, is a mixture of DNA from multiple sources...” (NRC I, 1992, p. 8)**

# Current Trends in Forensic DNA

- ***Faster results:*** Rapid DNA capabilities and new sample-to-answer integrated instruments
- ***Higher sensitivity:*** New assays lowering the limits of detection, which makes interpretation more challenging
- ***Higher information content:*** Next-generation sequencing (NGS) for more markers & STR allele information
- ***Stronger conclusions:*** Mixture interpretation with probabilistic genotyping models



# Forensic STR Sequence Diversity

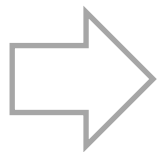


*Sequence-Based Heterozygote:* A locus that appears homozygous in length-based measurements (such as CE), but is heterozygous by sequence

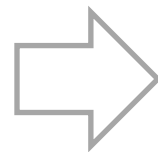
# Next Generation Sequencing (NGS)/ Massively Parallel Sequencing (MPS)

- **Higher information content** with sequence data
  - Expanded number of STR loci and other genetic markers such as SNPs and InDels
    - New markers may enable additional applications (e.g., biogeographical ancestry and phenotypic prediction)
  - **Deeper depth of information on STR alleles**
    - For example, eight different sequence versions of D12S391 alleles among 197 samples examined (Gelardi et al. 2014)
- **Significant challenges with BIG data**
  - STR allele nomenclature issues (ISFG DNA Commission - Parson et al. 2016)
  - Data storage (do you retain terabytes of data?)
  - Data analysis time will increase...
  - Privacy concerns with additional genomic information

True Sample  
Components



Sample  
Processing



DNA Data  
Obtained

Potential STR alleles

12 13 14 15 16 17 18 19



Total DNA amplified

4x

Genotype

13,17

female

13

17

Mixture Ratio of  
Components

1x

13

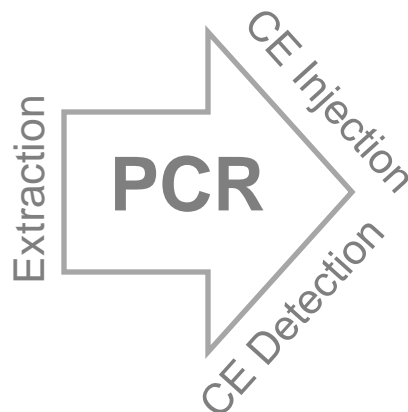
14

male

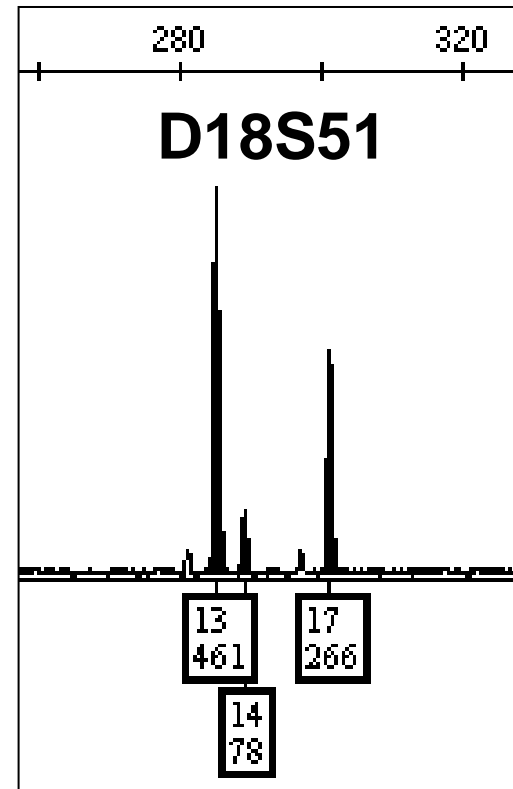
Potential Allele  
Overlap & Stacking

**Number of  
Contributors**  
(sample components)

**Validation**  
establishes variation  
and limits in the  
processes involved



portion of a CE  
electropherogram



**Infer possible genotypes &  
determine sample components**

From available data

**Goal of Interpretation**

# Updated Guidelines to Help with DNA Mixture Interpretation

Scientific Working Group on  
DNA Analysis Methods  
Interpretation Guidelines for  
Autosomal STR Typing  
by Forensic DNA Testing  
Laboratories



**Current guidelines are now 90 pages long  
and have examples**

**<https://www.swgdam.org/publication>**

# **5 Reasons that DNA Results Are Becoming More Challenging to Interpret**

- 1. More sensitive DNA test results**
- 2. More touch evidence samples** that are poor-quality, low-template, complex mixtures
- 3. More options exist** for statistical approaches involving probabilistic genotyping software
- 4. Many laboratories are not prepared** to cope with complex mixtures
- 5. More loci being added** because of the large number of samples in DNA databases



# Improved Sensitivity is a Two-Edged Sword

“As sensitivity of DNA typing improves, laboratories’ abilities to examine smaller samples increases. This improved sensitivity is a two-edged sword. **With greater capabilities comes greater responsibilities to report meaningful results.** Given the possibility of DNA contamination and secondary or even tertiary transfer in some instances, **does the presence of a single cell (or even a few cells) in an evidentiary sample truly have meaning?...**”

# More Touch Evidence Samples

<https://www.ncjrs.gov/pdffiles1/nij/grants/222318.pdf>

## The DNA Field Experiment: Cost-Effectiveness Analysis of the Use of DNA in the Investigation of High-Volume Crimes

John K. Roman  
Shannon Reid  
Jay Reid  
Aaron Chalfin  
William Adams  
Carly Knight

**Expanded DNA  
testing for  
burglary cases**

## NIJ April 2008 Research Report

<http://www.nij.gov/journals/261/pages/dna-solves-property-crimes.aspx>



DNA Solves Property Crimes (But Are We Ready for That?)  
by Nancy Ritter

**NIJ Journal October 2008** (vol. 261, pp. 2-12)

- **More poor-quality samples are being submitted**
  - Samples with <100 pg of DNA submitted in Belgium:  
**19% (2004) → 45% (2008)**  
(Michel 2009 FSIGSS 2:542-543)
- AAFS 2014 presentations showed poor success rates
  - NYC (A110): **only 10% of >9,500 touch evidence swabs from 2007 to 2011 produced usable DNA results**
  - Allegheny County (A114): examined touch DNA items processed from 2008 to 2013 across different evidence types (e.g., 6 of 56 car door handles yielded “resolvable profiles”)

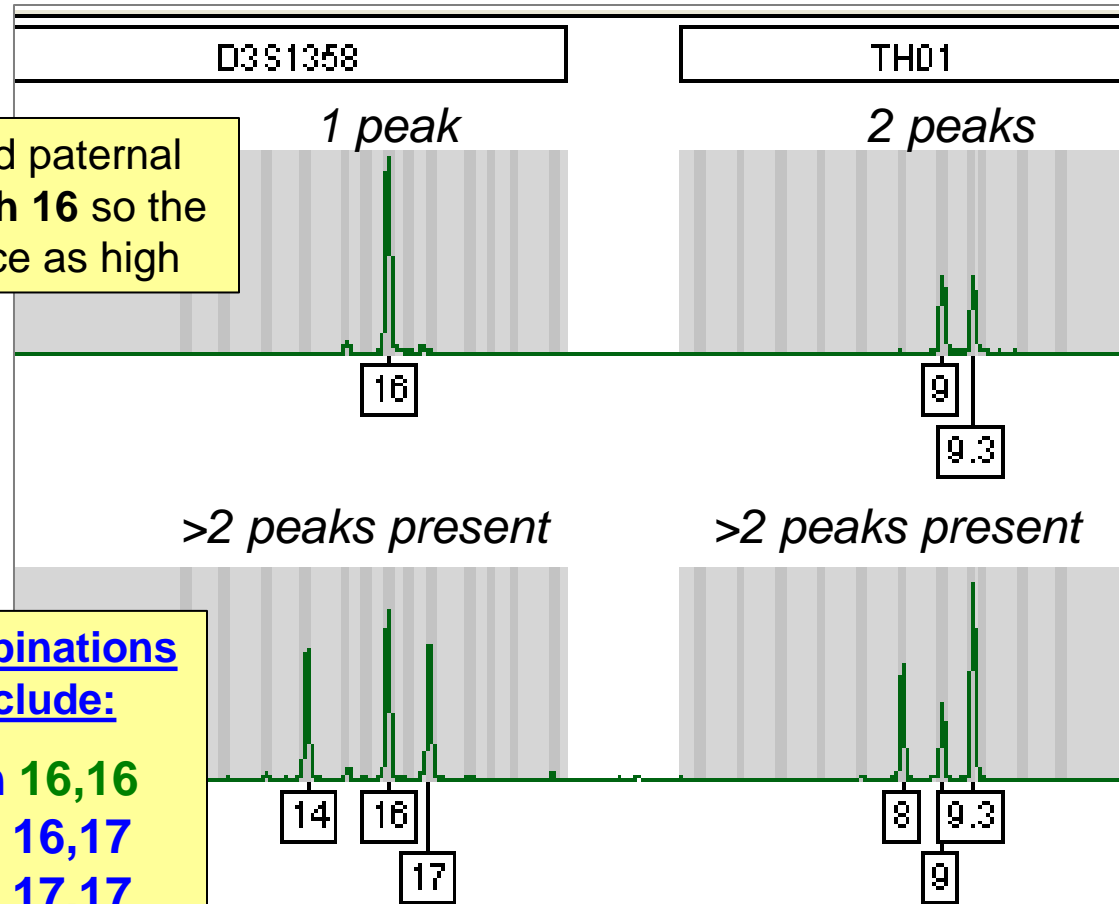
# New Options Exist for Statistical Analysis

- Increase in approaches to try and cope with potential allele dropout → number of **probabilistic genotyping** methods have grown since Balding & Buckleton 2009 article
- Many possible choices for **probabilistic genotyping software** with commercial interests at stake

Balding, D.J. & Buckleton, J. (2009) Interpreting low template DNA profiles. *Forensic Sci. Int. Genet.* 4(1):1-10.

Gill P, Whitaker J, Flaxman C, Brown N, Buckleton J. (2000) An investigation of the rigor of interpretation rules for STRs derived from less than 100 pg of DNA. *Forensic Sci. Int.* 112(1):17-40.

# Single-Source Sample vs Mixture Results



Single-Source

Mixture

Multiple possible combinations could have given rise to the mixture observed here

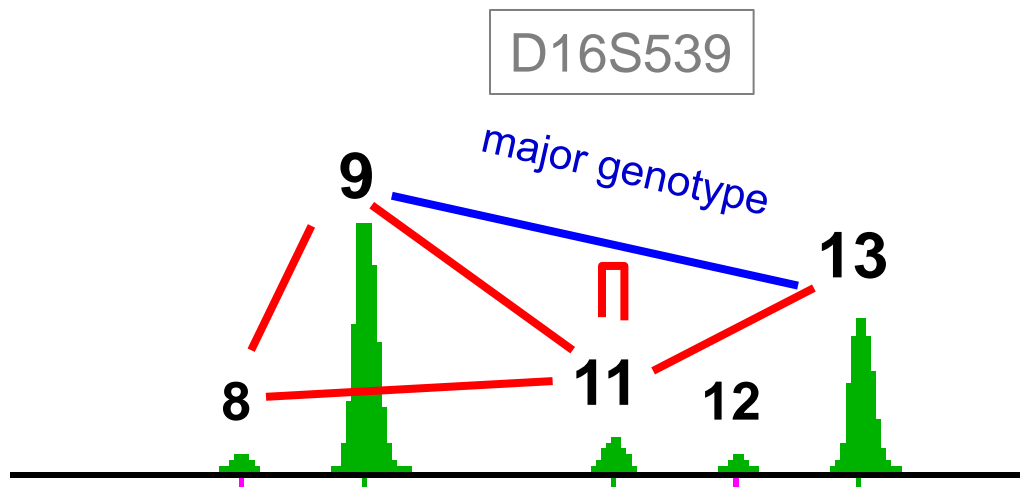
# Probabilistic Genotyping via Modeling Simulations

Mathematical Modeling  
of the Data

Typically thousands of  
simulations are performed  
→  
(MCMC)

Probable **Genotypes**  
to explain the mixture

PHR, mix ratio, stutter, etc...



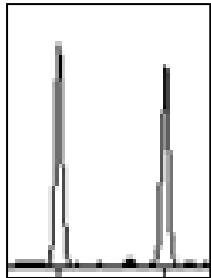
Minor Contributor Possible Genotypes	Probability
9,11	76%
11,11	15%
11,13	2%
8,11	2%
8,9	<1%
...	<1%

- Quantitative computer interpretation using numerous Markov Chain Monte Carlo (MCMC) simulations
- Models peak uncertainty and infers possible genotypes
- Results are presented as the Combined LR

# Math Analogy to DNA Evidence

$$2 + 2 = 4$$

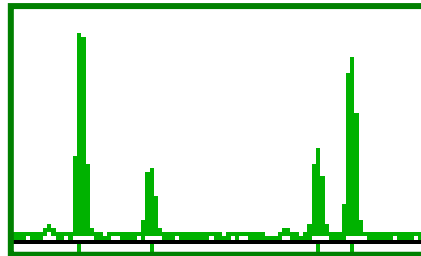
## Basic Arithmetic



**Single-Source  
DNA Profile**  
(DNA databasing)

$$2x^2 + x = 10$$

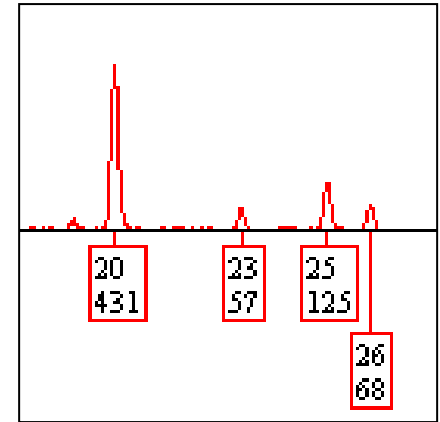
## Algebra



**Sexual Assault Evidence**  
(2-person mixture with  
high-levels of DNA)

$$\int_{x=0}^{\infty} f(x) dx$$

## Calculus



**Touch Evidence**  
(>2-person, low-level,  
complex mixtures  
perhaps involving  
relatives)



# Many laboratories are not prepared to cope with complex mixtures

- Have **appropriate validation studies** been performed to inform proper interpretation protocols? (curriculum & classroom instruction)
- Are **appropriately challenging proficiency tests** being given? (graded homework assignments)
- **Would we want to go into a calculus exam only having studied algebra and having completed homework assignments involving basic arithmetic?**

# Perhaps We Should Slow Down with Some of the DNA Mixtures That We (Scientists and Lawyers) Are Taking On...

## Poor Quality Conditions



## Large Numbers of Contributors



# The Future of Forensic DNA

is Similar to the Olympic Motto of  
“Faster, Higher, Stronger”



**Resources**

**Training**

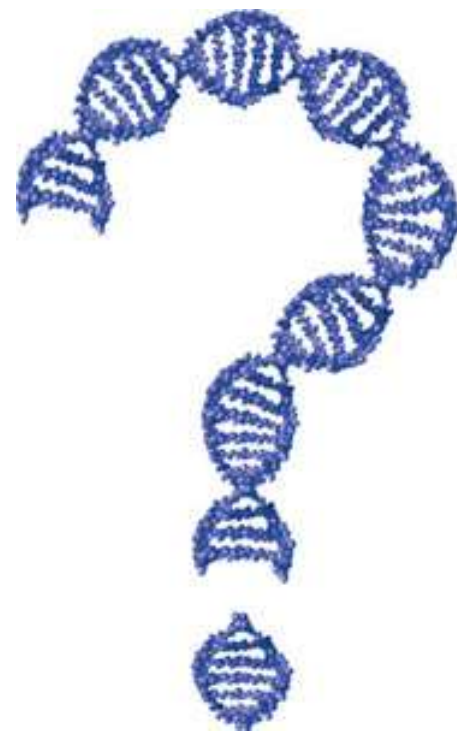
**Action**

**National Commission on Forensic Science (NCFS):**  
[www.justice.gov/ncfs](http://www.justice.gov/ncfs)

**Organization of Scientific Area Committees (OSAC):**  
[www.nist.gov/forensics/osac/index.cfm](http://www.nist.gov/forensics/osac/index.cfm)



[www.nist.gov/forensics](http://www.nist.gov/forensics)



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